

Ne-nen



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/724,209

DATE: 08/16/2004

TIME: 16:04:59

Input Set : N:\Crf4\Refhold\10_folder\J724209.raw
 Output Set: N:\CRF4\08162004\J724209.raw

1 <110> APPLICANT: ADLER, JON ELLIOT
 2 <120> TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
 3 <130> FILE REFERENCE: 100337.54075US
 4 <140> CURRENT APPLICATION NUMBER: US/10/724,209
 5 <141> CURRENT FILING DATE: 2003-12-01
 6 <150> PRIOR APPLICATION NUMBER: 60/195,532
 7 <151> PRIOR FILING DATE: 2000-04-07
 8 <150> PRIOR APPLICATION NUMBER: 60/247,014
 9 <151> PRIOR FILING DATE: 2000-11-13
 10 <160> NUMBER OF SEQ ID NOS: 31
 11 <170> SOFTWARE: PatentIn Ver. 2.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1002
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Homo sapiens
 17 <400> SEQUENCE: 1
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 20 ttttggatg tagtgaagag gcaggcaactg agcaacagtg atttgtgtct gctgtgtctc 180
 21 agcatcagcc ggctttcct gcatggactg ctgttcttga gtgctatcca gcttaccac 240
 22 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg 300
 23 attgcaaacc aaggcaacct ctggcttgct gcctgcctca gcctgctta ctgctccaag 360
 24 ctcatccgtt tcttcacac cttcctgatc tgcttggcaa gctgggtctc caggaagatc 420
 25 tcccagatgc tcctggat tattcttgc tcctgcatact gcaactgcct ctgtgtttgg 480
 26 tgcttttta gcagaccta cttcacagtc acaactgtgc tattcatgaa taacaataca 540
 27 aggctcaact ggcagattaa agatctcaat ttatttatt ctttcctt ctgctatctg 600
 28 tggctgtgc ctccttcct attgtttctg gtttcttctg ggatgctgac tgtctccctg 660
 29 ggaaggcaca tgaggacaat gaaggctat accagaaact ctcgtgaccc cagectggag 720
 30 gccccacatta aagccctcaa gtctttgtc tccttttct gtttcttctg gatatcatcc 780
 31 tgtgttgct tcatactctgt gcccctactg attctgtggc gcgacaaaat aggggtgatg 840
 32 gtttgtgttgg gataatggc agcttgcctc tctgggcattc cagccatct gatctcaggc 900
 33 aatgccaagt tgaggagagc tgtgtatgacc attctgtctt gggctcagag cagcctgaag 960
 34 gtaagagccg accacaaggc agattcccg acactgtgtct ga 1002
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 37 <211> LENGTH: 333
 38 <212> TYPE: PRT
 39 <213> ORGANISM: Homo sapiens
 40 <400> SEQUENCE: 2
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 42 1 5 10 15
 43 Thr Phe Leu Phe Ile Ser Val Leu Glu Phe Ala Val Gly Phe Leu Thr
 44 20 25 30
 45 Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln



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47 Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
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49 Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
50      65          70          75          80
51 Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
52      85          90          95
53 Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
54      100         105         110
55 Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
56      115         120         125
57 Leu Ile Cys Leu Ala Ser Trp Val Ser Arg Lys Ile Ser Gln Met Leu
58      130         135         140
59 Leu Gly Ile Ile Leu Cys Ser Cys Ile Cys Thr Val Leu Cys Val Trp
60      145         150         155         160
61 Cys Phe Phe Ser Arg Pro His Phe Thr Val Thr Thr Val Leu Phe Met
62      165         170         175
63 Asn Asn Asn Thr Arg Leu Asn Trp Gln Ile Lys Asp Leu Asn Leu Phe
64      180         185         190
65 Tyr Ser Phe Leu Phe Cys Tyr Leu Trp Ser Val Pro Pro Phe Leu Leu
66      195         200         205
67 Phe Leu Val Ser Ser Gly Met Leu Thr Val Ser Leu Gly Arg His Met
68      210         215         220
69 Arg Thr Met Lys Val Tyr Thr Arg Asn Ser Arg Asp Pro Ser Leu Glu
70      225         230         235         240
71 Ala His Ile Lys Ala Leu Lys Ser Leu Val Ser Phe Phe Cys Phe Phe
72      245         250         255
73 Val Ile Ser Ser Cys Val Ala Phe Ile Ser Val Pro Leu Leu Ile Leu
74      260         265         270
75 Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
76      275         280         285
77 Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
78      290         295         300
79 Arg Arg Ala Val Met Thr Ile Leu Leu Trp Ala Gln Ser Ser Leu Lys
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81 Val Arg Ala Asp His Lys Ala Asp Ser Arg Thr Leu Cys
82      325         330
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85 <211> LENGTH: 966
86 <212> TYPE: DNA
87 <213> ORGANISM: Homo sapiens
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91 atacatgcag ctgaatgggt tcaaaataag gcagtttcca caagtggcag gatcctgggt 180
92 ttccctgagtg tatccagaat agctctccaa agcctcatga tgtagaaat taccatcagc 240
93 tcaacctccc taagtttta ttctgaagac gctgttatatt atgcattcaa aataagttt 300
94 atattcttaa atttttgttag cctgtgtttt gtcgcctggc tcagtttctt ctactttgtg 360
95 aagattgcca atttctccta ccccccttttc ctcaaaactga ggtggagaat tactggattg 420

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96      ataccctggc ttctgtggct gtccgtgttt atttccttca gtcacagcat gttctgcata 480
97      aacatctgca ctgtgtattt taacaattct ttccctatcc actcctccaa ctccactaag 540
98      aaaacatact tgcgtgagat caatgtggc ggtctggct ttttctttaa cctggggatt 600
99      gtgactcctc tgatcatgtt catcctgaca gccaccctgc tgatcctctc tctcaagaga 660
100     cacaccctac acatggaaag caatgccaca gggtccaaacg accccagcat ggaggctcac 720
101     atgggggcca tcaaagctat cagctacttt ctcattctct acatttcaa tgcagttgct 780
102     ctgtttatct acctgtccaa catgtttgac atcaacagtc tgcgtgaaataa tttgtgccag 840
103     atcatcatgg ctgcctaccc tgccagccac tcaattctac tgattcaaga taaccctggg 900
104     ctgagaagag cctggaagcg gcttcagctt cgacttcatac ttatccccaa agagtggact 960
105     ctgtga                                         966

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108 <211> LENGTH: 321
109 <212> TYPE: PRT
110 <213> ORGANISM: Homo sapiens
111 <400> SEQUENCE: 4
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114     Ile Thr Leu Ile Leu Ala Val Leu Leu Ala Glu Tyr Leu Ile Gly Ile
115         20            25            30
116     Ile Ala Asn Gly Phe Ile Met Ala Ile His Ala Ala Glu Trp Val Gln
117         35            40            45
118     Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser Val
119         50            55            60
120     Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile Ser
121         65            70            75            80
122     Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala Phe
123         85            90            95
124     Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala Ala
125         100           105           110
126     Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
127         115           120           125
128     Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp Leu
129         130           135           140
130     Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys Ile
131         145           150           155           160
132     Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser Ser
133         165           170           175
134     Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly Leu
135         180           185           190
136     Ala Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe Ile
137         195           200           205
138     Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
139         210           215           220
140     Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His
141         225           230           235           240
142     Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
143         245           250           255
144     Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
145         260           265           270

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146 Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro Ala
147 275 280 285
148 Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg Ala
149 290 295 300
150 Trp Lys Arg Leu Gln Leu Arg Leu His Leu Tyr Pro Lys Glu Trp Thr
151 305 310 315 320
152 Leu
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155 <211> LENGTH: 972
156 <212> TYPE: DNA
157 <213> ORGANISM: Homo sapiens
158 <400> SEQUENCE: 5
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161 gccatctatg gggctgagtg ggccaggggc aaaacactcc ccactggta ccgcattatg 180
162 ttgatgctga gctttccag gctcttgcta cagatttggta tgatgctgga gaacattttc 240
163 agtctgctat tccgaattgt ttataaccaa aactcagttgt atatcctttt caaagtcatc 300
164 actgtcttcc tgaaccattc caatctctgg tttgctgcct qgctcaaagt cttctattgt 360
165 cttagaatttgc ctttttttgc ttcttcgttgc tgaagaggaa aatcatatgt 420
166 ctgtatgcctt ggcttctcag gctgtcagtg ttggtttccct taagcttcag ctttcctctc 480
167 tcgagagatg tcttcaatgt gtatgtaat agtccattc ctatcccctc ctccaactcc 540
168 acggagaaga agtacttctc tgagaccaat atggtaacc tggatattttt ctataacatg 600
169 gggatcttcg ttcctctgtat catgttcatc ctggcagcca ccctgctgtat cctctctctc 660
170 aagagacaca ccctcacat gggaaagcaat gccacagggt ccaggaccc cagcatgaag 720
171 gctcacatag gggccatcaa agccaccaggc tactttctca tcctctacat tttcaatgca 780
172 attgtcttat ttctttccac gtccaaacatc tttgacactt acagttcctg gaatattttg 840
173 tgcaagatca tcatggctgc ctaccctgccc ggccactcag tacaactgtat cttgggcaac 900
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178 <211> LENGTH: 323
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180 <213> ORGANISM: Homo sapiens
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185 20 25 30
186 Ile Leu Gly Ser Gly Phe Ile Thr Ala Ile Tyr Gly Ala Glu Trp Ala
187 35 40 45
188 Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
189 50 55 60
190 Phe Ser Arg Leu Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
191 65 70 75 80
192 Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
193 85 90 95
194 Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
195 100 105 110
196 Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His

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197	115	120	125
198	Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp		
199	130	135	140
200	Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu		
201	145	150	155
202	Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro		160
203	165	170	175
204	Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val		
205	180	185	190
206	Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met		
207	195	200	205
208	Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr		
209	210	215	220
210	Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys		
211	225	230	235
212	Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr		240
213	245	250	255
214	Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp		
215	260	265	270
216	Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr		
217	275	280	285
218	Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg		
219	290	295	300
220	Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly		
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222	Gln Thr Leu		320
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225 <211>	LENGTH: 930		
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231	atctcccttg ctgaccaaat tctcaactgct ctggcggtct ccagagttgg tttgctctgg 180		
232	gtattatttat taaaactggta ttcaactgtt tgaaatccag cttttaatag tgtagaagta 240		
233	agaactactg cttataatat ctgggcagtg atcaaccatt tcagcaactg gtttgcact 300		
234	acccttcagca tatttttattt gctcaagattt gccaattttt ccaactttat ttttcttac 360		
235	ttaaagagga gagttaaagag tgcattctg gtgatgttgg tggggcctt gctatttttgg 420		
236	gcttgcattc tttttgtat aaacatgaat gagattgtgc ggacaaaaaga atttgaaggaa 480		
237	aacatgactt ggaagatcaa attgaagagt gcaatgtact tttcaaatat gactgttaacc 540		
238	atggtagcaa acttagtacc cttcaactgtt accctactat cttttatgtt gttaatctgt 600		
239	tctttgttta aacatctcaa gaagatgcag ctccatggta aaggatctca agatcccagc 660		
240	accaagggtcc acataaaaagc tttgcaact gtgatctctt tcctcttggat atgtgccatt 720		
241	tactttctgt ccataatgtt atcagtttgg agttttggaa gtctggaaaa caaacctgtc 780		
242	ttcatgttct gcaaagctat tagattcagc tatccttcaa tccacccatt catcctgatt 840		
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244	gtgaaaaggag agaagacttc atctccatag		930
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247 <211>	LENGTH: 309		

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/16/2004
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Input Set : N:\Crf4\Refhold\10_folder\J724209.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; Xaa Pos. 2,3,4,6,7,10,13,18

Seq#:26; Xaa Pos. 1,2,3,5,6,13

Seq#:27; Xaa Pos. 3,4,5,7,8,10,12,13

Seq#:28; Xaa Pos. 3,8,11,12,13,16

Seq#:29; Xaa Pos. 4,8,10,11,12,13,14

Seq#:30; Xaa Pos. 3,4,7,8,10,13,14

VERIFICATION SUMMARY
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Input Set : N:\Crf4\Reffold\10_folder\J724209.raw
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843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
341 Repeated in SeqNo=25
880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
958 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
998 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
1037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0